IN THE CLAIMS

1. (currently amended) A method for detecting a mutation indicative of fragile X syndrome which is a disorder resulting from CGG repeat amplification in the FRAXA (FMR1) gene, which method comprises the steps of:

(a) obtaining genomic DNA to be tested,

(b) using PCR to amplify nucleic acid along the X-chromosome in the genomic DNA which includes all of the CGG repeats of the untranslated portion of the FRAXA gene plus a substantial contiguous segment of nucleic acid containing at least 21 nucleotides adjacent to said CGG repeats,

(c) obtaining single-stranded product from the amplified nucleic acid of step (b),

(d) hybridizing colorimetric-labeled oligonucleotides which separately target for (i) (CGG) repeats and (ii) said contiguous nucleic acid segment with said single-stranded product of step (c), <u>said target oligonucleotides for the CGG repeats containing between 3 and 7 triplets,</u>

(e) binding said single-stranded product of step (c) to a solid phase,

(f) separating said hybridized product of step (d) from the remainder of the target material,

(g) recovering the labeled target material from the separated product of step (f),

(h) then hybridizing the recovered labeled target material of step (g) to a microarray having a plurality of spots containing suitable oligonucelotide probes which

are separately complementary to said STR targets and to said contiguous nucleic acid segment targets, said CGG repeat probes containing between 6 and 20 triplets but at least twice as many triplets as said CGG repeat target oligonucleotides,

(i) following hybridization to the microarray, measuring the colorimetric intensities of said separately hybridized labeled target oligonucleotides present at specific spots on the microarray to obtain individual values therefor, and

(j) comparing the results of step (i) to determine the ratio of signal intensity at said STR probe spots to the signal intensity at said contiguous nucleic acid segment probe spots and then comparing such ratio with results from known control samples to accurately quantify the number of CGG repeats in the FRAXA gene of the obtained genomic DNA.

2. (currently amended) The method of claim 1 wherein the number of CGG repeats is determined using the following formula:

$N = 30 + (A - 1.03)66.4$ where N is the number of repeats and A is the ratio of the CI of the target oligonucleotides which hybridized with CGG probes to the CI of the target oligonucleotides which hybridized to the probes for the contiguous nucleic acid segment.

3. (previously presented) The method of claim 1 wherein said nucleic acid which is amplified includes the CGG repeat section on the X-chromosome and at least 21 nucleotides of the 3′ translated segment of the FRAXA gene.

4. canceled

5. (previously presented) The method of claim 1 wherein the labeled target oligonucleotides carry a fluorescent dye at 5′ end thereof.

6. (previously presented) The method of claim 1 wherein step (b) employs pairs of forward and reverse primers which are complementary to the 3′ borders of a DNA region that includes the entire CGG repeat section and said contiguous segment of the nucleic acid which contains at least 30 nucleotides.

7. (previously presented) The method of claim 6 wherein said contiguous segment is 3′ of the CGG repeat section and contains at least 30 nucleotides of the translated segment of the FRAXA gene.

8. (original) The method of claim 6 wherein the forward primer employed in step (b) which is complementary to the 3′ border of the antisense strand of the DNA region has an anchoring moiety at the 5′ end thereof.

9. (original) The method of claim 8 wherein the reverse primer has phosphate at its 5′ end and said single-stranded product obtained in step (c) is obtained

by digesting the antisense strand of the double-stranded PCR product with an exonuclease.

10. (original) The method of claim 9 wherein the anchoring moiety is biotin and wherein steps (e) and (f) are carried out following step (d) and separate said hybridized products by binding to avidin that is attached to a solid phase and washing.

11. (previously presented) The method of claim 10 wherein said labeled target material which hybridized in step (d) is recovered in step (g) separate from said single-stranded product by treating said hybridized product of step (d) to denature said strands and collecting the supernatant.

12. (original) The method of claim 9 wherein, following step (b), the amplified nucleic acid product is purified to remove unbound primers prior to treating with the exonuclease to obtain the single-stranded target material.

13. (original) The method of claim 6 wherein said forward primer includes SEQ ID NO: 1 and said reverse primer includes SEQ ID NO: 2.

14. (currently amended) A method for detecting a mutation indicative of fragile X syndrome which is a disorder resulting from CGG repeat amplification in the FRAXA (FMR1) gene, which method comprises the steps of:

(a) obtaining genomic DNA to be tested,

(b) using PCR and forward and reverse primers to amplify nucleic acid along the X-chromosome in the genomic DNA which includes all of the CGG repeats and a contiguous portion of the translated FRAXA gene including at least 21 nucleotides, said forward primers having an anchoring moiety at the 5′ end thereof,

(c) purifying the double-stranded product of step (b),

(d) obtaining single-stranded product from step (c) by digesting the antisense strand thereof with an exonuclease,

(e) hybridizing the product of step (d) with separate fluorescence-labeled antisense oligonucleotide targets for (CGG) repeats and for the contiguous portion of the FRAXA gene,

(f) separating said hybridized product of step (d) from the remainder of nonhybridized targets by binding to a solid phase through said anchoring moieties at the 5′ ends of said forward primers,

(g) hybridizing the labeled oligonucleotide targets obtained from the product of step (f) to a microarray containing suitable probes and, following hybridization to said microarray, measuring the fluorescent intensities of fluorescence-labeled target oligonucleotides present to obtain individual values for said (CGG) repeats and for said contiguous portion, and

(h) comparing the results of step (g) with results from known control samples using the following formula:

$N = 30 + (A - 1.03)66.4$ where N is the number of repeats and A is the ratio of the FI of the target oligonucleotides which hybridized with CGG probes to the FI of the target oligonucleotides which hybridized to the probes for the contiguous portion ~~segment~~, to accurately quantify the number of CGG repeats in the FRAXA gene of the DNA obtained.

15. (currently amended) A method for detecting a short tandem repeat polymorphism (STRP), which method comprises the steps of:

(a) obtaining genomic DNA to be tested,

(b) using PCR to amplify nucleic acid along the chromosome in the genomic DNA which includes all of the STRs of interest plus a substantial contiguous segment of the nucleic acid adjacent to said STRs which segment contains at least 21 nucleotides by employing a pair of forward and reverse primers which are complementary to the 3′ borders of a DNA region that includes the entire STR section and said contiguous segment of the nucleic acid which segment contains at least 30 nucleotides, said forward primer employed in step (b) being complementary to the 3′ border of the antisense strand of the DNA region and having an anchoring moiety at the 5′ end thereof, and the reverse primer having phosphate at its 5′ end,

(c) obtaining single-stranded product from the amplified DNA of step (b) by digesting the antisense strand of the double-stranded PCR product with an exonuclease,

(d) hybridizing different colorimetric-labeled oligonucleotides which separately target for (i) STRs and (ii) said contiguous nucleic acid segment with said single-stranded product of step (c), said labeled target oligonucleotides carrying fluorescent dye at 5′ ends thereof

(e) binding said single-stranded product of step (c) to a solid phase,

(f) separating said hybridized product of step (d) from the remainder of the labeled target material,

(g) recovering the labeled target oligonucleotides from the separated hybridized product of step (f),

(h) then hybridizing the recovered labeled target material of step (g) to a microarray having a plurality of spots containing suitable oligonucleotide probes which are complementary to said STR targets and to said contiguous nucleic acid segment targets,

(i) following hybridization to the microarray, measuring the colorimetric intensities of said separately hybridized labeled target oligonucleotides present at specific spots on the microarray to obtain individual values therefor, and

(j) comparing the results of step (i) to determine the ratio of signal intensity at said STR probe spots to the signal intensity at said contiguous nucleic acid segment probe spots and then comparing such ratio with results from known control samples to accurately quantify the number of STRs in the region of interest of the obtained DNA.

16. (previously presented) The method of claim 15 wherein the hybridizing target oligonucleotides for the STRs of step (d) contain between 3 and 7 repeats, and wherein the STR probes of step (h) contain between 6 and 20 repeats and at least twice as many repeats as said STR target oligonucleotides.

17-21 (canceled)

22. (currently amended) A method for detecting a mutation indicative of fragile X syndrome which is a disorder resulting from CGG repeat amplification in the FRAXA (FMR1) gene, which method comprises the steps of:

(a) obtaining genomic DNA to be tested,

(b) using PCR to amplify nucleic acid along the X-chromosome in the genomic DNA which includes all of the CGG repeats of the untranslated portion of the FRAXA gene plus a substantial contiguous segment of nucleic acid containing at least 21 nucleotides which is adjacent to said CGG repeats, such amplifying employing pairs of forward and reverse primers which are complementary to the 3′ borders of a DNA region that includes the entire CGG repeat section and said contiguous segment of the nucleic acid, which segment contains at least 30 nucleotides, wherein said forward primer includes SEQ ID NO: 1 and said reverse primer includes SEQ ID NO: 2,

(c) obtaining single-stranded product from the amplified nucleic acid of step (b) by digesting the antisense strands thereof,

(d) hybridizing colorimetric-labeled oligonucleotides, which separately target for (i) (CGG) repeats and (ii) said contiguous nucleic acid segment, with said single-stranded product of step (c),

(e) binding said single-stranded product of step (c) to a solid phase via anchoring moieties in a primer used in said PCR amplification of step (b),

(f) separating said hybridized product of step (d) from the remainder of the target material by washing said solid phase,

(g) recovering the labeled target material from the separated product of step (f) following the separation of said labeled target material from said single-stranded product,

(h) then hybridizing the recovered labeled target material of step (g) to a microarray having a plurality of spots containing suitable oligonucelotide probes which are separately complementary to said STR targets and to said contiguous nucleic acid segment targets,

(i) following hybridization to the microarray, measuring the colorimetric intensities of said separately hybridized labeled target oligonucleotides present at specific spots on the microarray to obtain individual values for said CGG ~~STR~~ targets and for said contiguous segment targets, and

(j) comparing the results of step (i) to determine the ratio of signal intensity at said CGG ~~STR~~ probe spots to the signal intensity at said contiguous nucleic acid segment probe spots and then comparing such ratio with results from known control

samples to accurately quantify the number of CGG repeats in the FRAXA gene of the obtained genomic DNA.

23. (currently amended) The method of claim 22 wherein the number of CGG repeats is determined in step (j) using the following formula:

$N = 30 + (A - 1.03)66.4$ where N is the number of repeats and A is the ratio of the CI of the target oligonucleotides which hybridized with CGG probes to the CI of the target oligonucleotides which hybridized to the probes for the contiguous nucleic acid segment.

24. (currently amended) The method of claim 22 wherein step (b) employs pairs of forward and reverse primers which ~~are complementary to the 3′ borders of a DNA region that includes the entire CGG repeat section and said contiguous segment of the nucleic acid, which segment contains at least 30 nucleotides, wherein said forward primer includes SEQ ID NO: 1 and said reverse primer includes SEQ ID NO: 2 and has~~ have phosphate at ~~its~~ the 5′ end, and wherein said digestion of the antisense in step (c) is with an exonuclease.

25. (currently amended) A method for detecting a mutation indicative of fragile X syndrome which is a disorder resulting from CGG repeat amplification in the FRAXA (FMR1) gene, which method comprises the steps of:

(a) obtaining genomic DNA to be tested,

(b) using PCR and forward and reverse primers to amplify nucleic acid along the X-chromosome in the genomic DNA which includes all of the CGG repeats and a contiguous segment of the translated FRAXA gene including at least 21 nucleotides, said forward primers having an anchoring moiety at the 5′ end thereof,

(c) purifying the double-stranded product of step (b),

(d) obtaining single-stranded product from step (c) by digesting the antisense strand thereof with an exonuclease,

(e) hybridizing the product of step (d) with separate fluorescence-labeled antisense oligonucleotide targets for (CGG) repeats and for the contiguous segment of the FRAXA gene,

(f) separating said hybridized product of step (d) from the remainder of nonhybridized targets by binding said single-stranded product to a solid phase through said anchoring moieties at the 5′ ends of said forward primers,

(g) then separating said labeled target oligonucleotides which had hybridized from said single-stranded product and hybridizing the separated labeled oligonucleotide targets to a microarray containing suitable probes and, following hybridization to said microarray, measuring the fluorescent intensities of fluorescence-labeled target oligonucleotides present to obtain individual values for said (CGG) repeats and for said contiguous segment ~~portion~~, and

(h) comparing the results of step (g) with results from known control samples to accurately quantify the number of CGG repeats in the FRAXA gene of the DNA obtained.